rm(list=ls(all=TRUE))

SeHEFA<-read.table("C:/Frontiers/R1/Data\_file\_S6.txt",header=TRUE,dec=",")

#install.packages("metafor",dep=TRUE)

library(metafor)

SeHEFA2 <- escalc("SMD",m1i=Hedgerow.Value,sd1i=Hedgerow.SD+0.1,n1i=nHedgerow,

m2i=Farmland.Value,sd2i=Farmland.SD+0.1,n2i=nControl,data=SeHEFA)

#Next line takes into account whether the relationship between effect size and observation is direct or inverse

SeHEFA2$yi<-SeHEFA2$yi\*SeHEFA2$New.sign

SeHEFA2$Ecosystem.Service<-factor(SeHEFA2$Ecosystem.Service,levels=c("Provisioning","Regulation","Support"))

SeHEFA2$New.Response<-factor(SeHEFA2$New.Response,levels=c("SoilF","Nitrogen","Phosphorus","Water","SoilR",

"Pests","Climate","Food"))

##Vote counting

nrow(SeHEFA2[SeHEFA2$yi<0,]) # Farmland better than hedgerows

nrow(SeHEFA2[SeHEFA2$yi>0,]) # Hedgerow better than farmland

nrow(SeHEFA2[SeHEFA2$yi==0,]) #Without hedgerows is similar as with hedgerows

##Null model

rem <- rma.mv(yi, vi, random = ~ 1 | Identifier, data=SeHEFA2)

rem # The difference is not significant(p=0.3607) and positive positiva (0.2998 +- 0.3280) #Without hedgerows is similar as with hedgerows

sav <- confint(rem)

W <- diag(1/SeHEFA2$vi)

X <- model.matrix(rem)

P <- W - W %\*% X %\*% solve(t(X) %\*% W %\*% X) %\*% t(X) %\*% W

100 \* sum(rem$sigma2) / (sum(rem$sigma2) + (rem$k-rem$p)/sum(diag(P))) # % heterogeneidad

100 \* sav$random[1,2:3] / (sav$random[1,2:3] + (rem$k-rem$p)/sum(diag(P))) # Intervalo de confianza del %

##Total I^2 is very high 96.29805 - 98.85578 % #### This justifies to include moderators

##Next lines select for relevant variables

datm <- SeHEFA2[,c(1,3,4,11,12,13,14,15,16)]

#and deletes rows with any NAs

datm <- datm[complete.cases(datm),]

rma.mv.Overall<-rma.mv(yi,vi,mods=~New.Response+Crop.type+

Climate.type+Spatial.Scale.Focus,random=~1|Identifier,data=datm)

summary(rma.mv.Overall)

rma.mv.New.Response<-rma.mv(yi,vi,mods=~0+New.Response,random=~1|Identifier,data=SeHEFA2)

summary(rma.mv.New.Response)

##Soil Formation versus following levels###

anova(rma.mv.New.Response, L=c(1,-1,0,0,0,0,0,0)) # (Q = 38.74, p < 0.01; significant; soil formation versus nitrogen cycling)

anova(rma.mv.New.Response, L=c(1,0,-1,0,0,0,0,0)) #(Q = 7.66, p < 0.01; significant; soil formation versus phosphorus cycling)

anova(rma.mv.New.Response, L=c(1,0,0,-1,0,0,0,0)) #(Q = 1.61, p = 0.20; non-significant; soil formation vs water regulation)

anova(rma.mv.New.Response, L=c(1,0,0,0,-1,0,0,0)) #(Q = 3.19, p = 0.07; non-significant; soil formation vs soil regulation)

anova(rma.mv.New.Response, L=c(1,0,0,0,0,-1,0,0)) #(Q = 0.19, p = 0.66; non-significant; soil formation vs pest regulation)

anova(rma.mv.New.Response, L=c(1,0,0,0,0,0,-1,0)) #(Q = 15.91, p < 0.01; significant; soil formation vs climate regulation)

anova(rma.mv.New.Response, L=c(1,0,0,0,0,0,0,-1)) #(Q = 47.45, p < 0.01; significant; soil formation vs food production)

###Nitrogen cycling versus following levels###

anova(rma.mv.New.Response, L=c(0,1,-1,0,0,0,0,0))#(Q = 66.06, p < 0.01; significant; nitrogen cycling vs phosphorus cycling)

anova(rma.mv.New.Response, L=c(0,1,0,-1,0,0,0,0))#(Q = 50.41, p < 0.01; significant; nitrogen cycling vs water regulation)

anova(rma.mv.New.Response, L=c(0,1,0,0,-1,0,0,0))#(Q = 2.35, p = 0.12; non-significant; nitrogen cycling vs soil regulation)

anova(rma.mv.New.Response, L=c(0,1,0,0,0,-1,0,0))#(Q = 5.12, p = 0.02; significant; nitrogen cycling vs pest regulation)

anova(rma.mv.New.Response, L=c(0,1,0,0,0,0,-1,0))#(Q = 7.59, p < 0.01; significant; nitrogen cycling vs climate regulation)

anova(rma.mv.New.Response, L=c(0,1,0,0,0,0,0,-1))#(Q = 20.65, p < 0.01; significant; nitrogen cycling vs food production)

###Phosphorus cycling versus following levels###

anova(rma.mv.New.Response, L=c(0,0,1,-1,0,0,0,0))#(Q = 2.57, p = 0.11; non-significant; phosphorus cycling vs water regulation)

anova(rma.mv.New.Response, L=c(0,0,1,0,-1,0,0,0))#(Q = 13.84, p < 0.01; significant; phosphorus cycling vs soil regulation)

anova(rma.mv.New.Response, L=c(0,0,1,0,0,-1,0,0))#(Q = 0.55, p = 0.46; non-significant; phosphorus cycling vs pest regulation)

anova(rma.mv.New.Response, L=c(0,0,1,0,0,0,-1,0))#(Q = 38.07, p < 0.01; significant; phosphorus cycling vs climate regulation)

anova(rma.mv.New.Response, L=c(0,0,1,0,0,0,0,-1))#(Q = 65.15, p < 0.01; significant; phosphorus cycling vs food production)

###Water regulation versus following levels######

anova(rma.mv.New.Response, L=c(0,0,0,1,-1,0,0,0))##(Q = 6.53, p = 0.01; significant; water regulation vs soil regulation)

anova(rma.mv.New.Response, L=c(0,0,0,1,0,-1,0,0))##(Q < 0.01, p = 0.99; non-significant; water regulation vs pest regulation)

anova(rma.mv.New.Response, L=c(0,0,0,1,0,0,-1,0))##(Q = 24.87, p < 0.01; significant; water regulation vs climate regulation)

anova(rma.mv.New.Response, L=c(0,0,0,1,0,0,0,-1))##(Q = 70.37, p < 0.01; significant; water regulation vs food production)

###Soil regulation versus following levels######

anova(rma.mv.New.Response, L=c(0,0,0,0,1,-1,0,0))##(Q = 2.16, p = 0.14; non-significant; soil regulation vs pest regulation)

anova(rma.mv.New.Response, L=c(0,0,0,0,1,0,-1,0))##(Q = 0.16, p = 0.69; non-significant; soil regulation vs climate regulation)

anova(rma.mv.New.Response, L=c(0,0,0,0,1,0,0,-1))##(Q = 22.43, p < 0.01; significant; soil regulation vs food production)

###Pest regulation versus following levels######

anova(rma.mv.New.Response, L=c(0,0,0,0,0,1,-1,0))##(Q = 2.77, p = 0.10; non-significant; pest regulation vs climate regulation)

anova(rma.mv.New.Response, L=c(0,0,0,0,0,1,0,-1))##(Q = 21.68, p < 0.01; significant; pest regulation vs food production)

###Climate regulation versus food provision#####

anova(rma.mv.New.Response, L=c(0,0,0,0,0,0,1,-1))##(Q = 28.15, p < 0.01; significant; climate regulation vs food production)

rma.mv.Farmland.type<-rma.mv(yi,vi,mods=~0+Farmland.type,random=~1|Identifier,data=SeHEFA2)

summary(rma.mv.Farmland.type)

anova(rma.mv.Farmland.type, L=c(1,-1)) # (Q = 22.0196, p < 0.01; significant)

rma.mv.Crop.type<-rma.mv(yi,vi,mods=~0+Crop.type,random=~1|Identifier,data=SeHEFA2)

summary(rma.mv.Crop.type)

anova(rma.mv.Crop.type, L=c(1,-1)) #(Q = 0.1934, p = 0.6601; non-significant)

rma.mv.Climate.type<-rma.mv(yi,vi,mods=~0+Climate.type,random=~1|Identifier,data=SeHEFA2)

summary(rma.mv.Climate.type)

anova(rma.mv.Climate.type, L=c(1,-1)) # (Q = 0.2368, p = 0.6265; non-significant)

rma.mv.Focus.of.spatial.scale<-rma.mv(yi,vi,mods=~0+Spatial.Scale.Focus,random=~1|Identifier,data=SeHEFA2)

summary(rma.mv.Focus.of.spatial.scale)

anova(rma.mv.Focus.of.spatial.scale, L=c(1,-1)) #(Q = 0.0901, p = 0.7641; non-significant)

datg1 <- as.data.frame(matrix(,nrow=8,ncol=6))

datg1[8,1] <- "aFood"

datg1[8,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Food"])

datg1[8,3] <- as.numeric(rma.mv.New.Response$beta[8])

datg1[8,4] <- as.numeric(rma.mv.New.Response$se[8])

datg1[8,5] <- as.numeric(rma.mv.New.Response$ci.lb[8])

datg1[8,6] <- as.numeric(rma.mv.New.Response$ci.ub[8])

datg1[7,1] <- "bClimate"

datg1[7,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Climate"])

datg1[7,3] <- as.numeric(rma.mv.New.Response$beta[7])

datg1[7,4] <- as.numeric(rma.mv.New.Response$se[7])

datg1[7,5] <- as.numeric(rma.mv.New.Response$ci.lb[7])

datg1[7,6] <- as.numeric(rma.mv.New.Response$ci.ub[7])

datg1[6,1] <- "cPests"

datg1[6,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Pests"])

datg1[6,3] <- as.numeric(rma.mv.New.Response$beta[6])

datg1[6,4] <- as.numeric(rma.mv.New.Response$se[6])

datg1[6,5] <- as.numeric(rma.mv.New.Response$ci.lb[6])

datg1[6,6] <- as.numeric(rma.mv.New.Response$ci.ub[6])

datg1[5,1] <- "dSoilR"

datg1[5,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="SoilR"])

datg1[5,3] <- as.numeric(rma.mv.New.Response$beta[5])

datg1[5,4] <- as.numeric(rma.mv.New.Response$se[5])

datg1[5,5] <- as.numeric(rma.mv.New.Response$ci.lb[5])

datg1[5,6] <- as.numeric(rma.mv.New.Response$ci.ub[5])

datg1[4,1] <- "eWater"

datg1[4,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Water"])

datg1[4,3] <- as.numeric(rma.mv.New.Response$beta[4])

datg1[4,4] <- as.numeric(rma.mv.New.Response$se[4])

datg1[4,5] <- as.numeric(rma.mv.New.Response$ci.lb[4])

datg1[4,6] <- as.numeric(rma.mv.New.Response$ci.ub[4])

datg1[3,1] <- "fPhosphorus"

datg1[3,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Phosphorus"])

datg1[3,3] <- as.numeric(rma.mv.New.Response$beta[3])

datg1[3,4] <- as.numeric(rma.mv.New.Response$se[3])

datg1[3,5] <- as.numeric(rma.mv.New.Response$ci.lb[3])

datg1[3,6] <- as.numeric(rma.mv.New.Response$ci.ub[3])

datg1[2,1] <- "gNitrogen"

datg1[2,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="Nitrogen"])

datg1[2,3] <- as.numeric(rma.mv.New.Response$beta[2])

datg1[2,4] <- as.numeric(rma.mv.New.Response$se[2])

datg1[2,5] <- as.numeric(rma.mv.New.Response$ci.lb[2])

datg1[2,6] <- as.numeric(rma.mv.New.Response$ci.ub[2])

datg1[1,1] <- "hSoilF"

datg1[1,2] <- length(SeHEFA2$New.Response[SeHEFA2$New.Response=="SoilF"])

datg1[1,3] <- as.numeric(rma.mv.New.Response$beta[1])

datg1[1,4] <- as.numeric(rma.mv.New.Response$se[1])

datg1[1,5] <- as.numeric(rma.mv.New.Response$ci.lb[1])

datg1[1,6] <- as.numeric(rma.mv.New.Response$ci.ub[1])

colnames(datg1) <- c("var","n","estimate","se","cil","ciu")

datg1$var <- as.factor(datg1$var)

#install.packages("ggplot2",dep=TRUE)

#install.packages("ggstance",dep=TRUE)

library(ggplot2)

library(ggstance)

plot <- ggplot(data=datg1, aes(y=var, x=estimate, xmin=datg1$cil,xmax=datg1$ciu))

mains <- plot + geom\_point(size = 2.5,fatten=2,position=position\_dodgev(height=0.60))+

geom\_errorbarh(aes(xmin=datg1$cil,

xmax=datg1$ciu),

size=1.1,position=position\_dodgev(height=0.60)) +

geom\_vline(aes(xintercept=0),linetype="dashed",colour="red")+

geom\_hline(aes(yintercept=1.5),colour="grey80")+

geom\_hline(aes(yintercept=5.5),colour="grey80")+

xlab(label = "Effect size") +

ylab(label = "") +

scale\_y\_discrete(labels=c("aFood"="Food production","bClimate"="Climate regulation",

"cPests"="Pest regulation","dSoilR"="Soil regulation","eWater"="Water regulation",

"fPhosphorus"="Phosphorus cycling",

"gNitrogen"="Nitrogen cycling","hSoilF"="Soil formation"))+

scale\_x\_continuous(limits=c(-2.5,2.8),breaks=c(-2,-1,0,1,2))+

geom\_text(x=-2.4,y=8,label = datg1[1,2],size=4)+

geom\_text(x=-2.4,y=7,label = datg1[2,2],size=4)+

geom\_text(x=-2.4,y=6,label = datg1[3,2],size=4)+

geom\_text(x=-2.4,y=5,label = datg1[4,2],size=4)+

geom\_text(x=-2.4,y=4,label = datg1[5,2],size=4)+

geom\_text(x=-2.4,y=3,label = datg1[6,2],size=4)+

geom\_text(x=-2.4,y=2,label = datg1[7,2],size=4)+

geom\_text(x=-2.4,y=1,label = datg1[8,2],size=4)+

theme\_bw()+

theme(legend.position="none")+

theme(panel.grid.major.y = element\_blank(), panel.grid.minor.y = element\_blank(),

panel.grid.major.x = element\_blank(), panel.grid.minor.x = element\_blank())+

theme(axis.text=element\_text(size=14),axis.title=element\_text(size=16,face="bold"))

mains

ggsave(filename="C:/Frontiers/R1/FigureS2.jpg",dpi = 1200, plot=mains, width = 120, height = 150, units = "mm")